

SEQUENCE LISTING

<110> Svendsen, Allan
Bisgard-Frantzen, Henrik
Borchert, Torben Vedel

<120> Alpha-Amylase Mutants

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<140> 09/327,563

<141> 1999-06-08

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aagtgaagaa gcagagaggc tattgaataa atgagtagaa gcgccatata ggcgcttttc   240
tttggaaga aaatatagggg aaaatggtac ttgttaaaaa ttcggaatat ttatacaaca   300
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ccc ccg gca tat aag gga acg agc caa gcg gat gtg ggc tac ggt gct 594
Pro Pro Ala Tyr Lys Gly Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala
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tac gac ctt tat gat tta ggg gag ttt cat caa aaa ggg acg gtt cgg 642
Tyr Asp Leu Tyr Asp Leu Gly Glu Phe His Gln Lys Gly Thr Val Arg
60 65 70

aca aag tac ggc aca aaa gga gag ctg caa tct gcg atc aaa agt ctt 690
Thr Lys Tyr Gly Thr Lys Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu
75 80 85 90

cat tcc cgc gac att aac gtt tac ggg gat gtg gtc atc aac cac aaa 738
His Ser Arg Asp Ile Asn Val Tyr Gly Asp Val Val Ile Asn His Lys
95 100 105

ggc ggc gct gat gcg acc gaa gat gta acc gcg gtt gaa gtc gat ccc 786
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110 115 120

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Ala Asp Arg Asn Arg Val Ile Ser Gly Glu His Leu Ile Lys Ala Trp
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aca cat ttt cat ttt ccg ggg cgc ggc agc aca tac agc gat ttt aaa 882
Thr His Phe His Phe Pro Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys
140 145 150

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Trp His Trp Tyr His Phe Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys
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Leu Asn Arg Ile Tyr Lys Phe Gln Gly Lys Ala Trp Asp Trp Glu Val
175 180 185

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Ser Asn Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp
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Tyr Asp His Pro Asp Val Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp
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tat gcc aat gaa ctg caa ttg gac ggt ttc cgt ctt gat gct gtc aaa 1122
Tyr Ala Asn Glu Leu Gln Leu Asp Gly Phe Arg Leu Asp Ala Val Lys
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His Ile Lys Phe Ser Phe Leu Arg Asp Trp Val Asn His Val Arg Glu
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Tyr Gly Asp Met Tyr Gly Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro
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415 420 425

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Gln Asn Ala Gly Glu Thr Trp His Asp Ile Thr Gly Asn Arg Ser Glu
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<213> B. licheniformis

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Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Thr Ser Gln
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Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu Phe
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His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Gly Glu Leu
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Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn Val Tyr Gly
115 120 125
Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr Glu Asp Val
130 135 140
Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val Ile Ser Gly
145 150 155 160
Glu His Leu Ile Lys Ala Trp Thr His Phe His Phe Pro Gly Arg Gly
165 170 175
Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly Thr
180 185 190
Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys Phe Gln Gly
195 200 205
Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn Tyr Asp Tyr
210 215 220
Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val Ala Ala Glu
225 230 235 240
Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln Leu Asp Gly
245 250 255
Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe Leu Arg Asp
260 265 270
Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met Phe Thr Val
275 280 285
Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn Tyr Leu Asn
290 295 300
Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu His Tyr Gln
305 310 315 320
Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met Arg Lys Leu
325 330 335

Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ser Val Thr Phe
 340 345 350
 Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr Val
 355 360 365
 Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg Glu
 370 375 380
 Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys Gly
 385 390 395 400
 Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro Ile
 405 410 415
 Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His Asp Tyr Phe
 420 425 430
 Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser Val
 435 440 445
 Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly Ala
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 Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr Trp His Asp
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 ggggggttgt tattatttta ctgatatgta aaatataatt tgtataagaa aatgagaggg 240
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Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser			
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Asp Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu			
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agc caa tcc gat aac gga tac gga cct tat gat ttg tat gat tta gga 531			
Ser Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly			
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gaa ttc cag caa aaa ggg acg gtc aga acg aaa tac ggc aca aaa tca 579			
Glu Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser			
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Tyr Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu			
100	105	110	
gat gta act gcc gtc gaa gtc aat ccg gcc aat aga aat cag gaa act 723			
Asp Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr			
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Ser Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly			
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Arg Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp			
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Arg Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly
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195 200 205

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210 215 220

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260 265 270

aac tac ttg aat aaa aca agc ttt aat caa tcc gtg ttt gat gtt ccg 1203
Asn Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val Pro
275 280 285

ctt cat ttc aat tta cag gcg gct tcc tca caa gga ggc gga tat gat 1251
Leu His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr Asp
290 295 300

atg agg cgt ttg ctg gac ggt acc gtt gtg tcc agg cat ccg gaa aag 1299
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305 310 315

gcg gtt aca ttt gtt gaa aat cat gac aca cag ccg gga cag tca ttg 1347
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Glu Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile
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Gly Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn
370 375 380

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Ile Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro Gln
385 390 395

cac gat tat att gac cac ccg gat gtg atc gga tgg acg agg gaa ggt 1587
His Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly
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gac agc tcc gcc gcc aaa tca ggt ttg gcc gct tta atc acg gac gga 1635
Asp Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly
420 425 430

ccc ggc gga tca aag cgg atg tat gcc ggc ctg aaa aat gcc ggc gag 1683
Pro Gly Gly Ser Lys Arg Met Tyr Ala Gly Leu Lys Asn Ala Gly Glu
435 440 445

aca tgg tat gac ata acg ggc aac cgt tca gat act gta aaa atc gga 1731
Thr Trp Tyr Asp Ile Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly
450 455 460

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Ser Asp Gly Trp Gly Glu Phe His Val Asn Asp Gly Ser Val Ser Ile
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Tyr Val Gln Lys
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Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp Ile
50 55 60
Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser Gln
65 70 75 80
Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu Phe
85 90 95
Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu Leu
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Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr Gly
115 120 125
Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp Val
130 135 140
Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser Glu
145 150 155 160
Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg Gly
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Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly Ala
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Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg Gly
195 200 205
Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn Tyr
210 215 220
Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val Val
225 230 235 240
Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser Leu
245 250 255
Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe Leu
260 265 270
Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met Phe
275 280 285
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 Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Tyr Asp Met Arg
 325 330 335
 Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu Lys Ala Val
 340 345 350
 Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser
 355 360 365
 Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr
 370 375 380
 Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr
 385 390 395 400
 Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn Ile Glu
 405 410 415
 Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro Gln His Asp
 420 425 430
 Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp Ser
 435 440 445
 Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly
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 Gly Ser Lys Arg Met Tyr Ala Gly Leu Lys Asn Ala Gly Glu Thr Trp
 465 470 475 480
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 Val Leu Thr Phe His Arg
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 Thr Leu Trp Thr Lys Val Ala Asn Glu Ala Asn Asn Leu Ser Ser Leu
 25 30 35

ggc atc acc gct ctt tgg ctg ccg ccc gct tac aaa gga aca agc cgc 413
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 40 45 50

agc gac gta ggg tac gga gta tac gac ttg tat gac ctc ggc gaa ttc 461
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 55 60 65

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 Asp Ala Val Glu Val Asn Pro Ser Asp Arg Asn Gln Glu Ile Ser Gly
 120 125 130

acc tat caa atc caa gca tgg acg aaa ttt gat ttt ccc ggg cgg ggc 701
Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe Asp Phe Pro Gly Arg Gly
135 140 145

aac acc tac tcc agc ttt aag tgg cgc tgg tac cat ttt gac ggc gtt 749
Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp Tyr His Phe Asp Gly Val
150 155 160

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Asp Trp Asp Glu Ser Arg Lys Leu Ser Arg Ile Tyr Lys Phe Arg Gly
165 170 175 180

atc ggc aaa gcg tgg gat tgg gaa gta gac acg gaa aac gga aac tat 845
Ile Gly Lys Ala Trp Asp Trp Glu Val Asp Thr Glu Asn Gly Asn Tyr
185 190 195

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Asp Tyr Leu Met Tyr Ala Asp Leu Asp Met Asp His Pro Glu Val Val
200 205 210

acc gag ctg aaa aac tgg ggg aaa tgg tat gtc aac aca acg aac att 941
Thr Glu Leu Lys Asn Trp Gly Lys Trp Tyr Val Asn Thr Thr Asn Ile
215 220 225

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Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe Phe
230 235 240

cct gat tgg ttg tgg tat gtg cgt tct cag act ggc aag ccg cta ttt 1037
Pro Asp Trp Leu Ser Tyr Val Arg Ser Gln Thr Gly Lys Pro Leu Phe
245 250 255 260

acc gtc ggg gaa tat tgg agc tat gac atc aac aag ttg cac aat tac 1085
Thr Val Gly Glu Tyr Trp Ser Tyr Asp Ile Asn Lys Leu His Asn Tyr
265 270 275

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Ile Thr Lys Thr Asp Gly Thr Met Ser Leu Phe Asp Ala Pro Leu His
280 285 290

aac aaa ttt tat acc gct tcc aaa tca ggg ggc gca ttt gat atg cgc 1181
Asn Lys Phe Tyr Thr Ala Ser Lys Ser Gly Gly Ala Phe Asp Met Arg
295 300 305

acg tta atg acc aat act ctc atg aaa gat caa ccg aca ttg gcc gtc 1229

Thr Leu Met Thr Asn Thr Leu Met Lys Asp Gln Pro Thr Leu Ala Val
310 315 320

acc ttc gtt gat aat cat gac acc gaa ccc ggc caa gcg ctg cag tca 1277
Thr Phe Val Asp Asn His Asp Thr Glu Pro Gly Gln Ala Leu Gln Ser
325 330 335 340

tgg gtc gac cca tgg ttc aaa ccg ttg gct tac gcc ttt att cta act 1325
Trp Val Asp Pro Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr
345 350 355

cgg cag gaa gga tac ccg tgc gtc ttt tat ggt gac tat tat ggc att 1373
Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr Gly Asp Tyr Tyr Gly Ile
360 365 370

cca caa tat aac att cct tcg ctg aaa agc aaa atc gat ccg ctc ctc 1421
Pro Gln Tyr Asn Ile Pro Ser Leu Lys Ser Lys Ile Asp Pro Leu Leu
375 380 385

atc gcg cgc agg gat tat gct tac gga acg caa cat gat tat ctt gat 1469
Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr Gln His Asp Tyr Leu Asp
390 395 400

cac tcc gac atc atc ggg tgg aca agg gaa ggg ggc act gaa aaa cca 1517
His Ser Asp Ile Ile Gly Trp Thr Arg Glu Gly Gly Thr Glu Lys Pro
405 410 415 420

gga tcc gga ctg gcc gca ctg atc acc gat ggg ccg gga gga agc aaa 1565
Gly Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly Ser Lys
425 430 435

tgg atg tac gtt ggc aaa caa cac gct gga aaa gtg ttc tat gac ctt 1613
Trp Met Tyr Val Gly Lys Gln His Ala Gly Lys Val Phe Tyr Asp Leu
440 445 450

acc ggc aac cgg agt gac acc gtc acc atc aac agt gat gga tgg ggg 1661
Thr Gly Asn Arg Ser Asp Thr Val Thr Ile Asn Ser Asp Gly Trp Gly
455 460 465

gaa ttc aaa gtc aat ggc ggt tcg gtt tcg gtt tgg gtt cct aga aaa 1709
Glu Phe Lys Val Asn Gly Gly Ser Val Ser Val Trp Val Pro Arg Lys
470 475 480

acg acc gtt tct acc atc gct cgg ccg atc aca acc cga ccg tgg act 1757
Thr Thr Val Ser Thr Ile Ala Arg Pro Ile Thr Thr Arg Pro Trp Thr

ggt gaa ttc gtc cgt tgg acc gaa cca cgg ttg gtg gca tgg cct 1802
Gly Glu Phe Val Arg Trp Thr Glu Pro Arg Leu Val Ala Trp Pro
505 510 515

tgatgcctgc ga 1814

<210> 6
<211> 549
<212> PRT
<213> B. stearothermophilus

<400> 6

Val Leu Thr Phe His Arg Ile Ile Arg Lys Gly Trp Met Phe Leu Leu
1 5 10 15

Ala Phe Leu Leu Thr Val Ser Leu Phe Cys Pro Thr Gly Gln Pro Ala
20 25 30

Lys Ala Ala Ala Pro Phe Asn Gly Thr Met Met Gln Tyr Phe Glu Trp
35 40 45

Tyr Leu Pro Asp Asp Gly Thr Leu Trp Thr Lys Val Ala Asn Glu Ala
50 55 60

Asn Asn Leu Ser Ser Leu Gly Ile Thr Ala Leu Trp Leu Pro Pro Ala
65 70 75 80

Tyr Lys Gly Thr Ser Arg Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu
85 90 95

Tyr Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr
100 105 110

Gly Thr Lys Ala Gln Tyr Leu Gln Ala Ile Gln Ala Ala His Ala Ala
115 120 125

Gly Met Gln Val Tyr Ala Asp Val Phe Asp His Lys Gly Gly Ala
130 135 140

Asp Gly Thr Glu Trp Val Asp Ala Val Glu Val Asn Pro Ser Asp Arg
145 150 155 160

Asn Gln Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe
165 170 175

Asp Phe Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp
180 185 190

Tyr His Phe Asp Gly Val Asp Trp Asp Glu Ser Arg Lys Leu Ser Arg
195 200 205

Ile Tyr Lys Phe Arg Gly Ile Gly Lys Ala Trp Asp Trp Glu Val Asp
210 215 220

Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Leu Asp Met
225 230 235 240

Asp His Pro Glu Val Val Thr Glu Leu Lys Asn Trp Gly Lys Trp Tyr

245 250 255
 Val Asn Thr Thr Asn Ile Asp Gly Phe Arg Leu Asp Ala Val Lys His
 260 265 270
 Ile Lys Phe Ser Phe Phe Pro Asp Trp Leu Ser Tyr Val Arg Ser Gln
 275 280 285
 Thr Gly Lys Pro Leu Phe Thr Val Gly Glu Tyr Trp Ser Tyr Asp Ile
 290 295 300
 Asn Lys Leu His Asn Tyr Ile Thr Lys Thr Asp Gly Thr Met Ser Leu
 305 310 315 320
 Phe Asp Ala Pro Leu His Asn Lys Phe Tyr Thr Ala Ser Lys Ser Gly
 325 330 335
 Gly Ala Phe Asp Met Arg Thr Leu Met Thr Asn Thr Leu Met Lys Asp
 340 345 350
 Gln Pro Thr Leu Ala Val Thr Phe Val Asp Asn His Asp Thr Glu Pro
 355 360 365
 Gly Gln Ala Leu Gln Ser Trp Val Asp Pro Trp Phe Lys Pro Leu Ala
 370 375 380
 Tyr Ala Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr
 385 390 395 400
 Gly Asp Tyr Tyr Gly Ile Pro Gln Tyr Asn Ile Pro Ser Leu Lys Ser
 405 410 415
 Lys Ile Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr
 420 425 430
 Gln His Asp Tyr Leu Asp His Ser Asp Ile Ile Gly Trp Thr Arg Glu
 435 440 445
 Gly Gly Thr Glu Lys Pro Gly Ser Gly Leu Ala Ala Leu Ile Thr Asp
 450 455 460
 Gly Pro Gly Gly Ser Lys Trp Met Tyr Val Gly Lys Gln His Ala Gly
 465 470 475 480
 Lys Val Phe Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile
 485 490 495
 Asn Ser Asp Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser
 500 505 510
 Val Trp Val Pro Arg Lys Thr Thr Val Ser Thr Ile Ala Arg Pro Ile
 515 520 525
 Thr Thr Arg Pro Trp Thr Gly Glu Phe Val Arg Trp Thr Glu Pro Arg
 530 535 540
 Leu Val Ala Trp Pro
 545

<210> 7

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Mutagenesis primer

<400> 7

ggtcgtaggc accgtagccc caatccgctt g

31

<210> 8

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Mutagenesis primer

<400> 8

ggtcgtaggc accgtagccc caatcccatt ggctcg

36

<210> 9

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Mutagenesis Primer

<400> 9

ctgtgactgg tgagtactca accaagtc

28

<210> 10

<211> 478

<212> PRT

<213> A. oryzae

<400> 10

Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr Phe Leu Leu Thr

1 5 10 15

Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala Thr Cys Asn Thr

20 25 30

Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly Ile Ile Asp Lys

35 40 45

Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Thr Pro

50 55 60

Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly Asp Ala Tyr His

65 70 75 80

Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu Asn Tyr Gly Thr

85	90	95
Ala Asp Asp Leu Lys	Ala Leu Ser Ser	Ala Leu His Glu Arg Gly Met
100	105	110
Tyr Leu Met Val Asp	Val Val Ala Asn His	Met Gly Tyr Asp Gly Ala
115	120	125
Gly Ser Ser Val Asp	Tyr Ser Val Phe Lys	Pro Phe Ser Ser Gln Asp
130	135	140
Tyr Phe His Pro Phe	Cys Phe Ile Gln Asn	Tyr Glu Asp Gln Thr Gln
145	150	155
Val Glu Asp Cys Trp	Leu Gly Asp Asn Thr	Val Ser Leu Pro Asp Leu
165	170	175
Asp Thr Thr Lys Asp	Val Val Lys Asn Glu	Trp Tyr Asp Trp Val Gly
180	185	190
Ser Leu Val Ser Asn	Tyr Ser Ile Asp Gly	Leu Arg Ile Asp Thr Val
195	200	205
Lys His Val Gln Lys	Asp Phe Trp Pro Gly	Tyr Asn Lys Ala Ala Gly
210	215	220
Val Tyr Cys Ile Gly	Glu Val Leu Asp Gly	Asp Pro Ala Tyr Thr Cys
225	230	235
Pro Tyr Gln Asn Val	Met Asp Gly Val Leu	Asn Tyr Pro Ile Tyr Tyr
245	250	255
Pro Leu Leu Asn Ala	Phe Lys Ser Thr Ser	Gly Ser Met Asp Asp Leu
260	265	270
Tyr Asn Met Ile Asn	Thr Val Lys Ser Asp	Cys Pro Asp Ser Thr Leu
275	280	285
Leu Gly Thr Phe Val	Glu Asn His Asp Asn	Pro Arg Phe Ala Ser Tyr
290	295	300
Thr Asn Asp Ile Ala	Leu Ala Lys Asn Val	Ala Ala Phe Ile Ile Leu
305	310	315
Asn Asp Gly Ile Pro	Ile Ile Tyr Ala Gly	Gln Glu Gln His Tyr Ala
325	330	335
Gly Gly Asn Asp Pro	Ala Asn Arg Glu Ala	Thr Trp Leu Ser Gly Tyr
340	345	350
Pro Thr Asp Ser Glu	Leu Tyr Lys Leu Ile	Ala Ser Ala Asn Ala Ile
355	360	365
Arg Asn Tyr Ala Ile	Ser Lys Asp Thr Gly	Phe Val Thr Tyr Lys Asn
370	375	380
Trp Pro Ile Tyr Lys	Asp Asp Ile Thr Ile	Ala Met Arg Lys Gly Thr
385	390	395
Asp Gly Ser Gln Ile	Val Thr Ile Leu Ser	Asn Lys Gly Ala Ser Gly
405	410	415
Asp Ser Tyr Thr Leu	Ser Leu Ser Gly Ala	Gly Tyr Thr Ala Gly Gln
420	425	430
Gln Leu Thr Glu Val	Ile Gly Cys Thr Thr	Val Thr Val Gly Ser Asp
435	440	445

Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro Arg Val Leu Tyr
 450 455 460
 Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser Ser Ser
 465 470 475

<210> 11
 <211> 1458
 <212> DNA
 <213> Bascillius

<220>
 <221> CDS
 <222> (1)...(1455)

<400> 11
 cat cat aat gga aca aat ggt act atg atg caa tat ttc gaa tgg tat 48
 His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
 1 5 10 15

ttg cca aat gac ggg aat cat tgg aac agg ttg agg gat gac gca gct 96
 Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala
 20 25 30

aac tta aag agt aaa ggg ata aca gct gta tgg atc cca cct gca tgg 144
 Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp
 35 40 45

aag ggg act tcc cag aat gat gta ggt tat gga gcc tat gat tta tat 192
 Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
 50 55 60

gat ctt gga gag ttt aac cag aag ggg acg gtt cgt aca aaa tat gga 240
 Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
 65 70 75 80

aca cgc aac cag cta cag gct gcg gtg acc tct tta aaa aat aac ggc 288
 Thr Arg Asn Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly
 85 90 95

att cag gta tat ggt gat gtc gtc atg aat cat aaa ggt gga gca gat 336
 Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
 100 105 110

ggt acg gaa att gta aat gcg gta gaa gtg aat cgg agc aac cga aac 384
 Gly Thr Glu Ile Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn

115	120	125	
cag gaa acc tca gga gag tat gca ata gaa gcg tgg aca aag ttt gat 432			
Gln Glu Thr Ser Gly Glu Tyr Ala Ile Glu Ala Trp Thr Lys Phe Asp			
130	135	140	
ttt cct gga aga gga aat aac cat tcc agc ttt aag tgg cgc tgg tat 480			
Phe Pro Gly Arg Gly Asn Asn His Ser Ser Phe Lys Trp Arg Trp Tyr			
145	150	155	160
cat ttt gat ggg aca gat tgg gat cag tca cgc cag ctt caa aac aaa 528			
His Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Gln Leu Gln Asn Lys			
165	170	175	
ata tat aaa ttc agg gga aca ggc aag gcc tgg gac tgg gaa gtc gat 576			
Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp			
180	185	190	
aca gag aat ggc aac tat gac tat ctt atg tat gca gac gtg gat atg 624			
Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met			
195	200	205	
gat cac cca gaa gta ata cat gaa ctt aga aac tgg gga gtg tgg tat 672			
Asp His Pro Glu Val Ile His Glu Leu Arg Asn Trp Gly Val Trp Tyr			
210	215	220	
acg aat aca ctg aac ctt gat gga ttt aga ata gat gca gtg aaa cat 720			
Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His			
225	230	235	240
ata aaa tat agc ttt acg aga gat tgg ctt aca cat gtg cgt aac acc 768			
Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr			
245	250	255	
aca ggt aaa cca atg ttt gca gtg gct gag ttt tgg aaa aat gac ctt 816			
Thr Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu			
260	265	270	
ggt gca att gaa aac tat ttg aat aaa aca agt tgg aat cac tcg gtg 864			
Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His Ser Val			
275	280	285	
ttt gat gtt cct ctc cac tat aat ttg tac aat gca tct aat agc ggt 912			
Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly			
290	295	300	

ggg tat tat gat atg aga aat att tta aat ggt tct gtg gtg caa aaa 960
Gly Tyr Tyr Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gln Lys
305 310 315 320

cat cca aca cat gcc gtt act ttt gtt gat aac cat gat tct cag ccc 1008
His Pro Thr His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
325 330 335

ggg gaa gca ttg gaa tcc ttt gtt caa caa tgg ttt aaa cca ctt gca 1056
Gly Glu Ala Leu Glu Ser Phe Val Gln Gln Trp Phe Lys Pro Leu Ala
340 345 350

tat gca ttg gtt ctg aca agg gaa caa ggt tat cct tcc gta ttt tat 1104
Tyr Ala Leu Val Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
355 360 365

ggg gat tac tac ggt atc cca acc cat ggt gtt ccg gct atg aaa tct 1152
Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser
370 375 380

aaa ata gac cct ctt ctg cag gca cgt caa act ttt gcc tat ggt acg 1200
Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr Gly Thr
385 390 395 400

cag cat gat tac ttt gat cat cat gat att atc ggt tgg aca aga gag 1248
Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu
405 410 415

gga aat agc tcc cat cca aat tca ggc ctt gcc acc att atg tca gat 1296
Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
420 425 430

ggg cca ggt ggt aac aaa tgg atg tat gtg ggg aaa aat aaa gcg gga 1344
Gly Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys Asn Lys Ala Gly
435 440 445

caa gtt tgg aga gat att acc gga aat agg aca ggc acc gtc aca att 1392
Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile
450 455 460

aat gca gac gga tgg ggt aat ttc tct gtt aat gga ggg tcc gtt tcg 1440
Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser
465 470 475 480

gtt tgg gtg aag caa taa
Val Trp Val Lys Gln
485

1458

<210> 12
<211> 485
<212> PRT
<213> Bascillius

<400> 12

His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
1 5 10 15
Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala
20 25 30
Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp
35 40 45
Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
50 55 60
Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
65 70 75 80
Thr Arg Asn Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly
85 90 95
Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
100 105 110
Gly Thr Glu Ile Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn
115 120 125
Gln Glu Thr Ser Gly Glu Tyr Ala Ile Glu Ala Trp Thr Lys Phe Asp
130 135 140
Phe Pro Gly Arg Gly Asn Asn His Ser Ser Phe Lys Trp Arg Trp Tyr
145 150 155 160
His Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Gln Leu Gln Asn Lys
165 170 175
Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp
180 185 190
Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met
195 200 205
Asp His Pro Glu Val Ile His Glu Leu Arg Asn Trp Gly Val Trp Tyr
210 215 220
Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
225 230 235 240
Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr
245 250 255
Thr Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
260 265 270

Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His Ser Val
 275 280 285
 Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly
 290 295 300
 Gly Tyr Tyr Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gln Lys
 305 310 315 320
 His Pro Thr His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
 325 330 335
 Gly Glu Ala Leu Glu Ser Phe Val Gln Gln Trp Phe Lys Pro Leu Ala
 340 345 350
 Tyr Ala Leu Val Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
 355 360 365
 Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser
 370 375 380
 Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr Gly Thr
 385 390 395 400
 Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu
 405 410 415
 Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
 420 425 430
 Gly Pro Gly Gly Asn Lys Trp Met Tyr Val Gly Lys Asn Lys Ala Gly
 435 440 445
 Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile
 450 455 460
 Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser
 465 470 475 480
 Val Trp Val Lys Gln
 485

<210> 13
 <211> 483
 <212> PRT
 <213> Bascillius

<400> 13
 Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp
 1 5 10 15
 Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
 20 25 30
 Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser
 35 40 45
 Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
 50 55 60
 Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu
 65 70 75 80

Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr
 85 90 95
 Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp
 100 105 110
 Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser
 115 120 125
 Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg
 130 135 140
 Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
 145 150 155 160
 Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg
 165 170 175
 Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn
 180 185 190
 Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val
 195 200 205
 Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser
 210 215 220
 Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe
 225 230 235 240
 Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met
 245 250 255
 Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu Glu Asn
 260 265 270
 Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val Pro Leu
 275 280 285
 His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr Asp Met
 290 295 300
 Arg Lys Leu Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ser
 305 310 315 320
 Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
 325 330 335
 Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
 340 345 350
 Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
 355 360 365
 Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile
 370 375 380
 Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His
 385 390 395 400
 Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp
 405 410 415
 Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
 420 425 430
 Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr

435 440 445
 Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
 450 455 460
 Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr
 465 470 475 480
 Val Gln Arg

<210> 14
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Substitution sequences

<400> 14
 Ile Pro Thr His Ser Val
 1 5

<210> 15
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Substitution sequences

<400> 15
 Ile Pro Thr His Gly Val
 1 5

<210> 16
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Substitution sequences

<400> 16
 Ile Pro Gln Tyr Asn Ile
 1 5